BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.1 [Aug-1-2001]

Matrix [BLOSUM62 ▼] gap open: [11] gap extension: [1]

x_dropoff: [15] expect: [10.00] wordsize: [3] Filter ☑

Sequence 1 lcl|seq_1 Length 510 (1 .. 510)

Sequence 2 lcl|seq_2 Length 512 (1 .. 512)

2

NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 786 bits (2029), Expect = 0.0
Identities = 419/522 (80%), Positives = 448/522 (85%), Gaps = 22/522 (4%)

```
Query:   1  MFIESFRVESPHVRYGAAEIESDYQYDTTELVHESHDGASRWIVRPKSVRYNFRTTTTVP   SEQ ID2
        60
            MFIESFRVESPHVRYGAAEIES+Y+YDTTELVHESHDGASRW+VRPKSV+Y+FRT+TTVP
Sbjct:   1  MFIESFRVESPHVRYGAAEIESEYRYDTTELVHESHDGASRWVVRPKSVQYHFRTSTTVP   SEQ ID3
        60

Query:  61  KLGVMLVGWGGNNGSTLTAGVIANREGISWATKDKVQQANYYGSLTQASTIRVGSYNGEE   SEQ ID2
       120
            KLGVMLVGWGGNNGSTLTAGVIA+REGISWATKDKVQQANYYGSLTQASTIRVGSYNGEE
Sbjct:  61  KLGVMLVGWGGNNGSTLTAGVIASREGISWATKDKVQQANYYGSLTQASTIRVGSYNGEE   SEQ ID3
       120

Query: 121  IYAPFKSLLPMVNPDDLVFGGWDISNMNLADAMTRAKVLDIDLQKQLRPYMES-------   SEQ ID2
       173
            IYAPFKSLLPMVNPDDLVFGGWDISNMNLADAMTRAKVLDIDLQKQLRPYMES
Sbjct: 121  IYAPFKSLLPMVNPDDLVFGGWDISNMNLADAMTRAKVLDIDLQKQLRPYMESWCLSLAS   SEQ ID3
       180

Query: 174  MVPL--PGIYDPDVIAANQGSRANNVIKGTKKEQMEQIIKDIREFKEKSKVDKVVVLWTA   SEQ ID2
       231
            M+P   P  DP  A   SR          ++ +  +  KDIREFKE +K+DK VVLWTA
Sbjct: 181  MIPTSSPLTRDP---ARTMSSRE------PRRSRWGRSSKDIREFKEHNKMDKAVVLWTA   SEQ ID3
       231
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Fig: 1

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Query: 232 NTERYSN-VCVGLNDTMENLLASVDKHEAEISPSTLYAIACV-MEGIPFIIIGSPQNTFVP      SEQ ID2
289

            NTERY+N +C+GL  T      ASVD+N+AEISPSTLY        +EG+  + G+ +      P

Sbjct: 232 NTERYNHCLCLGLM-TNGKPSASVDRNQAEISPSTLYCHCLASLEGVRSITGALKKKSWP      SEQ ID3
290


Query: 290 GLIDLAIKNNCLI-GGDDFKSGQTKMKSVLVDFLVGAGIKPTSIVSYNHLGNNDGHNLSA      SEQ ID2
348

            G+ DLAIK      GG   K G+ K K+ LVDFL+GAGIKPTSIVSYNHLGNN DG NLSA

Sbjct: 291 GIDDLAIKKKLPDPGGLIQKRGKPKKKTGLVDFLMGAGIKPTSIVSYNHLGNNDGTNLSA      SEQ ID3
350


Query: 349 PQTFRSKEISKSNVVDDMVSSNAILYELGEHPDHVVVIKYVPYVGDSKRAMDEYTSEIFM      SEQ ID2
408

            PQTFRSKEISKS+VVDDMVSSNAILYE GEHPDHVVVIKYVPYVGDSKRAMDEYTSEIFM

Sbjct: 351 PQTFRSKEISKSSVVDDMVSSNAILYEPGEHPDHVVVIKYVPYVGDSKRAMDEYTSEIFM      SEQ ID3
410


Query: 409 GGKSTIVLHHTCEDSLLAAPIILDLVLLAELSTRIQLKAEGEEKFHSFHPVATILSYLTK      SEQ ID2
468

            GGK+TIVLHHTCEDSLLAAPIILDLVLLAELSTRIQLK EGEEKFHSFHPVATILSYLTK

Sbjct: 411 GGKNTIVLHHTCEDSLLAAPIILDLVLLAELSTRIQLKGEGEEKFHSFHPVATILSYLTK      SEQ ID3
470


Query: 469 APLVPPGTPVVNALAKQRAMLENIMRACVGLAPENNMILEYK 510·                  SEQ ID2
            APLVPPGTPVVNALAKQRAMLENIMRACVGLAPENNMILEYK

Sbjct: 471 APLVPPGTPVVNALAKQRAMLENIMRACVGLAPENNMILEYK 512                  SEQ ID3
CPU time:     0.10 user secs.      0.02 sys. secs         0.12 total
secs.


Gapped
Lambda     K        H
   0.316    0.134    0.385


Gapped
Lambda     K        H
   0.267   0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 2125
Number of Sequences: 0
Number of extensions: 153
Number of successful extensions: 5
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 510
length of database: 233,319,389
effective HSP length: 125
effective length of query: 385
effective length of database: 176,133,389
effective search space: 67811354765
effective search space used: 67811354765
```

Fig: 1 (Cont'd)